

O I P E

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PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Lechler, Robert
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION

<130> 02292/000H795-US0

<140> US 09/674,462
<141> 2001-05-08

<150> PCT/GB99/01350
<151> 1999-04-30

<150> GB-9809280.2
<151> 1998-04-30

<160> 35

<170> PatentIn Ver. 2.1

<210> 1
<211> 223
<212> PRT
<213> Sus scrofa

<400> 1

Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 2
<211> 672

<212> DNA

<213> Sus scrofa

<400> 2

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ccctgtacag ctctgtttc tcttctcttc atccctgtct tctccaaagg gatgcacgtg 120
gcccacacccg cagtagtgc ggcacacagg cgggggtttt ccagctttgt gtgtgagttt 180
gggtctgcag gcaaaagctgc cgaggccgg gtgacagttgc tgcggccggc cggcagccag 240
atgactgaag tctgtgcccgc gacatataact gtggaggatg agttgacctt ccttcatgac 300
tctacatgca ctggcacccctc caccgaaaac aaagtgaacc tcaccatcca agggctgaga 360
gccgtggaca ctgggcttc catctgcaag gtggagctcc tgtaccacc accctactat 420
gtgggtatgg gcaacgggac ccagattttt gtcattgtatc cagaaccatg cccagattt 480
gattttctgc tctggatcctt ggcagcagttt agttcaggtt tttttttttt cagttccctc 540
atcacagctg tttcttttagt caaaatgcta aagaaaagaa gtcctttaac tacaggggtc 600
tatgtgaaaaa tgccccccgac agagccagaa tgtgaaaagc aatttcagcc ttattttattt 660
cccatcaattt ga 672

<210> 3

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pCTLA4-Ig construct (Figure 4)

<400> 3

Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
2

145	150	155	160												
Asp	Gly	Gly	Ser	Gly	Gly	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
				165				170					175		
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
				180				185				190			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				195				200			205				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
				210		215						220			
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				225		230				235			240		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
				245				250			255				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
				260				265				270			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
				275				280				285			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				290		295					300				
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
				305		310				315			320		
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
				325				330			335				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
				340				345				350			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
				355				360			365				
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				370		375				380					
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
				385		390				395			400		

<210> 4
 <211> 722
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 4
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 ttcctgtgc agcctctgga ttcacctta gcagctatgc catgagctgg gtccgcagg 120
 ctccagggaa ggggctggag tgggtcttag ctattcgtgg tagtgggtggt agcacatact 180
 acgcagactc cgtgaagggc cggttccacca tctccagaga caattccaag aacacgtgt 240
 atctgcaat gaacagccctg agagccgagg acacggccgt gtattactgt gcaagagctg 300
 gtcgtatccc gtttgactat tggggccaag gtaccctggc caccgtctcg agtgggtggag 360
 gcggttcagg cggaggtggc tctggcgta gtgcacttca gtctgtgctg actcagccac 420

cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctgga agcagctcca 480
acatcggaa taattatgtt tactggtaacc agcagctccc aggaacggcc cccaaactcc 540
tcatctatag gaataatcg cggcccttag gggccctgaa ccgattctct ggctccaagt 600
ctggcaccc tcgacccctg gccatcgtg ggctccggcc cgaggatgag gctgattatt 660
actgtgcagc atggatgac agcctggat tcggcggagg gaccaagctc accgtccctag 720
gt 722

<210> 5
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Phage library

<400> 5
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly 15
1 5 10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 30
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45
35 40 45
Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val 60
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95
85 90 95
Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 110
100 105 110
Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly 125
115 120 125
Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly 140
130 135 140
Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn 160
145 150 155 160
Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala 175
165 170 175
Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro 190
180 185 190
Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile 205
195 200 205
Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp 220
210 215 220
Asp Asp Ser Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly 240
225 230 235 240

<210> 6

<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Phage library

<400> 6
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ccaggctcca gggaaaggggc tggagtggtt ctcagctatt agtggtagtg gtggtagcac 180
atactacgca gactccgtga aggccgggtt caccatctcc agagacaatt ccaagaacac 240
gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtcaag 300
agctggctgt attttgtttt actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
tggaggcggt tcaggcggag gtggctctgg cggttagtgca cttcagtgctg tgctgactca 420
gccaccctca gcgtctggga ccccccggca gagggtcacc atctttgtt ctggaaagcag 480
ctccaaacatc ggaagtaatt atgtatactg gtaccagcag cttccaggaa cggcccccaa 540
actcctcatc tataggaata atcagcggcc ctcaagggtc cctgaccgat tctctggctc 600
caagcttggc acctcagcct ccctggccat cagtggttgc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct ggtattcggc ggagggacca agctgaccgt 720
ccttaggtgc 729

<210> 7
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> Phage library

<400> 7
catggccgag gtgcagctgc aggagtcggg cccaggactg gtgaagcctc gggagaccct 60
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ccggcagccc ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac 180
caactacaac ccctccctca agagtcgagt caccatatac gttagacacgt ccaagaacca 240
gttctccctg aagctgagct ctgtgaccgc tgccggacacg gccgtgtatt actgtcaag 300
aatgcggaaag gataagttt actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
tggagggcgt tcaggcggag gtggctctgg cggttagtgca cttcagtgctg tgctgactca 420
gccaccctca gcgtctggga ccccccggca gagggtcacc atctttgtt ctggaaagcag 480
ctccaaacatc ggaagtaatt atgtatactg gtaccagcag cttccaggaa cggcccccaa 540
actcctcatc tataggaata atcagcggcc ctcaagggtc cctgaccgat tctctggctc 600
caagcttggc acctcagcct ccctggccat cagtggttgc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct gtttgattc ggcggaggaa ccaagctgac 720
cgtccttaggt gcggccgc 738

<210> 8
<211> 739
<212> DNA
<213> Artificial Sequence

<220>
<223> Phage library

<400> 8
catggccgag gtgcagctgg tgcagtctgg ggctgagtga agaggccggg ggcctcagt 60
aaggtttcct gcaaggcatc tggatcaccc ttccacagct actatatgca ctgggtgcga 120
caggccccctg gacaagggtt tgagtggatg ggaataatca acccttagtg tggttagcac 180
caagctacgc acagaagttc cagggcagag tcaccatgac caggacacg tccacgagca 240
cagtctacat ggagctgagc agcctgagat ctgaggacac ggccgtgtat tactgtca 300
gaatggctcc ctatgtaat acgcttgttt tttggggccat agtaccctg gtcaccgtct 360
cgagttgtgg aggccgttca ggcggagggtg gctctggcgg tagtgcactt cagtctgtgc 420
tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc acatgccaag 480

taggagacag cctcagaagc tattatgaa gctggatcca gcagaagcca ggacaggccc 540
ctgtacttgt catctatggt aaaaacaacc ggccctcagg gatcccagac cgattcttg 600
gctccagtc agaaacaca gcttccttga ccatcactgg ggctcaggcg gaagatgagg 660
ctgacttta ctgttaactcc cgggacagca gtggtttac tgtattcggc ggagggacca 720
agctgaccgt ccttaggtgc 739

<210> 9
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Phage library

<400> 9
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tgaagatctc ctgttaagggt tctggataca gctttaccag ctactggatc ggctgggtgc 120
gccagatgcc cgggaaaggc ctggagtggta tggggatcat ctatcctgt gactctgata 180
ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag tccatcagca 240
ccgcctacct gcagtggagc agcctgaagg cctcggacac ggcctgttat tactgtgcaa 300
gatttcgcgt tgggtttt gactattggg gccaaggatc cctggtcacc gtctcgagtg 360
gtggaggcgg ttcaggcggta ggtggctctg gcggtagtgc acttgacatc cagttgaccc 420
agtctccatg ttcctgtctg catctgttagg agacagatc accatcactt gccggggcag 480
tcagggcatt agcagtatt tagcctggta tcagaaaaaa ccagggaaag cccctaagct 540
cctggcttat gctgcatcca ctttgcggaa tggggtccca tcaaggatc gcggcagtgg 600
atctggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660
ttactgtcaa cagcttaata gttaccgctt gacgttcggc caagggacca agctggaaat 720
caaacgtgc 729

<210> 10
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Phage library

<400> 10
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly
 130 135 140
 Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
 145 150 155 160
 Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 165 170 175
 Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro
 180 185 190
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
 195 200 205
 Ser Gly Leu Arg Ser Glu Asp Glu Ala Ser Tyr Tyr Cys Ala Ala Trp
 210 215 220
 Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 225 230 235 240

<210> 11
 <211> 246
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Phage library

<400> 11
 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
 1 5 10 15
 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Val Ser
 20 25 30
 Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 35 40 45
 Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
 50 55 60
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser
 130 135 140
 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser
 145 150 155 160
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro
 165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser
180 185 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
195 200 205

Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val
210 215 220

Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala
245

<210> 12

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Phage library

<400> 12

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val
130 135 140

Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
145 150 155 160

Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175

Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
180 185 190

Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
195 200 205

Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg
8

210

215

220

Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Gly Thr Lys Leu Thr Val
225 230 235 240

Leu Gly

<210> 13

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Phage library

<400> 13

Gln Val Gln Leu Leu Gln Ser Ala Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gln Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
145 150 155 160

Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
165 170 175

Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn
210 215 220

Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
225 230 235 240

<210> 14

<211> 742
<212> DNA
<213> Homo sapiens

<400> 14
agcttcagga tcctgaaagg ttttgctcta cttcctgaag acctgaacac cgctccata 60
aagccatggc ttgccttgc tttcagcggc acaaggctca gctgaacctg gctaccagga 120
cctggccctg cactctcctg tttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180
acgtggccca gcctgctgtg gtactggcca gcagccgagg catccgcagc tttgtgtgt 240
agtatgcac tccaggcaaa gccactgagg tccgggtgac agtgcctcg caggctgaca 300
gccagggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagtt accttcctag 360
atgattccat ctgcacgggc acctccagtg gaaatcaagt gaacctcaact atccaaggac 420
tgagggccat ggacacggga ctctacatct gcaaggtgga gctcatgtac ccaccggcat 480
actacccctggg cataggcaac ggaacccaga tttatgtaat tcatccagaa ccgtgcccag 540
attctgactt ctcctctgg atccttgcag cagttatcc ggggtgttt ttttatact 600
ttctcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660
gggtctatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720
ttatcccattt caatttgagaa tt 742

<210> 15
<211> 223
<212> PRT
<213> Homo sapiens

<400> 15
Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15
Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 16
<211> 773
<212> DNA
<213> Homo sapiens

<400> 16
aagcttcgag ccaaggcagcg tcctggggag cgcgtcatgg ccttaccagt gaccgccttg 60
ctccgtccgc tggccttgc gctccacgccc gcccaggccgaa gcccaggcttccgg ggtgtcgccg 120
ctggatcgaa cctggaaacctt gggcgagaca gtggagctga agtgcgcagggt gctgctgtcc 180
aacccgacgt cgggctgctc gtggcttcc cagccgcgcg gcccgcgc cagtcacc 240
ttccctctat acctctccca aaacaagccc aaggcgcccg agggtctgaa caccaggcgg 300
ttctcggca agaggttggg ggacacaccc ttgcctcacc ttgcactt cccgcggagag 360
aacgagggtc actatttcgt ctcggccctg agcaactcca tcatgtactt cagccacttc 420
gtgcccgtct tcctgccagc gaagccacc accgacgcagg cggccgcacc accaacaccg 480
gcccacca tcgcgtcgc gcccgttcc ctgcgcggccagg aggctgtccgg gccagcggcg 540
ggggcgcgcg tgcacacggg ggggttggac ttgcctgtt atatctacat ctggcgcggcc 600
ttggccggaa cttgtgggtt ctttccttgc tcactggta tcaccctta ctgcaaccac 660
aggaaccgaa gacgtgtttt caaatgtccc cggcctgtgg tcaaatcgaa agacaagccc 720
agccttcgg cgagatacgt ctaaccctgt gcaacagccca ctacatgaat tcc 773

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
ttgaagctta gccatggctt gctctgga 28

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
taatgaattc tcaattgatg ggaataaaat aag 33

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
cggttctgca gcaccaccgg agccaccatc agaatctggg catggttctg gatcaatgac 60

<210> 20
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
gagctgaaac gggcggccgc agaac 25

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
ctggccttgca gcattcagat cc 22

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
ttcaaagctt caggatcctg aaaggtttg 30

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
taatgaattc tcaatttgatg ggaataaaat aag 33

<210> 24
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 24
gatgttagata tcacaggcga agtcgacacc accggagcca ccaattacat aaatctggc 60
tccgttgct atgccc 76

<210> 25
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 25
tcgcgc ccaa gcttcg agcc aagc a g c g t 29

<210> 26
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
taatgaattc tcaattgatg ggaataaaat aag 33

<210> 27
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 27
cataggcaac ggagcccaga tttatgtaat tgg tggctcc ggtgggtcg acttcgcctg 60
tgatatctac atc 73

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: linker

<400> 28
Gly Gly Ser Gly Gly Ala Ala
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: hexapeptide motif

<400> 29
Met Tyr Pro Pro Pro Tyr
1 5

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: hexapeptide motif

<400> 30

Leu Tyr Pro Pro Pro Tyr
1 5

<210> 31

<211> 223

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15

Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140

Asn Gly Ala Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 32

<211> 221

<212> PRT

<213> Bos taurus

<400> 32

Met Ala Cys Ser Gly Phe Gln Ser His Gly Thr Trp Trp Thr Ser Arg
1 5 10 15

Thr	Trp	Pro	Cys	Thr	Ala	Leu	Phe	Phe	Leu	Val	Phe	Ile	Pro	Val	Phe
				20				25				30			
Ser	Lys	Gly	Met	Asn	Val	Thr	Gln	Pro	Pro	Val	Val	Leu	Ala	Ser	Ser
				35			40				45				
Arg	Gly	Val	Ala	Ser	Phe	Ser	Cys	Glu	Tyr	Glu	Ser	Ser	Gly	Lys	Ala
				50		55			60						
Asp	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Glu	Ala	Gly	Ser	Gln	Val	Thr
	65			70				75						80	
Glu	Val	Cys	Ala	Gly	Thr	Tyr	Met	Val	Glu	Asp	Glu	Leu	Thr	Phe	Leu
				85				90					95		
Asp	Asp	Ser	Thr	Cys	Ile	Gly	Thr	Ser	Arg	Gly	Asn	Lys	Val	Asn	Leu
				100				105					110		
Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Val	Cys	Lys
				115			120					125			
Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Val	Gly	Ile	Gly	Asn	Gly
				130		135					140				
Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	Phe
	145				150					155					160
Leu	Leu	Trp	Ile	Leu	Ala	Ala	val	Ser	Ser	Gly	Leu	Phe	Phe	Tyr	Ser
				165				170					175		
Phe	Leu	Ile	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys	Arg	Ser
				180				185					190		
Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu	Pro	Glu
				195		200						205			
Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn			
				210		215					220				

<210> 33
<211> 672
<212> DNA
<213> *Homo sapiens*

<400> 33	atggcttgc	ttggatttca	gcggcacaag	gctcagctga	acctggctgc	caggacctgg	60
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	gcccagcctg	ctgtggta	ggccagcagc	cgaggcatcg	ccagcttgt	gtgtgatgtat	180
	gcatctccag	gcaaagccac	tgaggtccgg	gtgacagtgc	ttcggcaggc	tgacagccag	240
	gtgactgaag	tctgtgcggc	aacctacatg	atggggaaatg	agttgacctt	cctagatgtat	300
	tccatctgca	ccggcacctc	cagtggaaat	caagtgaacc	tcactatcca	aggactgagg	360
	gccatggaca	cgggactcta	catctgcaag	gtggagctca	tgtacccacc	gccatactac	420
	ctgggcata	gcaacggagc	ccagatttat	gtaattgatc	cagaaccgtg	cccagattct	480
	gacttcctcc	tctggatcct	tgcagcagtt	agttcggggt	tgtttttta	tagcttctc	540
	ctcacagctg	tttctttgag	caaaatgcta	aagaaaagaa	gccctttac	aacaggggtc	600
	tatgtaaaaa	tggcccaac	agagccagaa	tgtaaaagc	aatttcagcc	ttattttatt	660
	cccatcaatt	qa					672

<210> 34
<211> 666
<212> DNA

<213> Bos taurus

<400> 34

atggcttgct ctggattcca gagtcatggg acttgggtgga catctaggac ctggccctgc 60
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cctccagtgg tgctggctag cagccggggt gttgccagct tctcatgtga atatgagtc 180
tcaggcggaa ctgacgaggc ccgggtgaca gtgctgcggg aggcaggcag ccaggtgacc 240
gaagtcgtg ctgggaccta catgggtggag gatgagctaa ccttcctgga tgattccact 300
tgcattggca cctccagagg aaacaaagtg aacctcacca tccaaagggtc gagggccatg 360
gacactgggc tctatgtctg caaagtggag ctcatgttacc cgccgcctca ctacgtggc 420
atcggaatg gaacccagat ttacgtcatt gatccagaac catgcccggaa ttctgatttt 480
ctcctctgga tcctggcagc agttagttca gggttgttt tctacagctt cctcatcaca 540
gctgtttctt tgagcaaaat gctaaagaaa agaagccctc ttactacagg ggtctatgtg 600
aaaatgcccc caacagagcc agaatgtgaa aagcaatttc agccttattt tattcccatc 660
aattga 666

<210> 35

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker

<400> 35

Gly Gly Ser Gly Gly
1 5